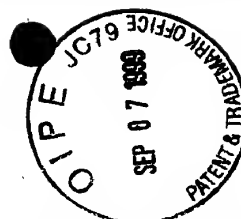


SEQUENCE LISTING



<110> Yamamoto, Hiroaki

<120> METHOD FOR PRODUCING OPTICALLY ACTIVE 4-HALO-3-HYDROXYBUTYRIC ACID ESTER

<130> 06501/030001

<150> JP 1998-126507

<151> 1998-10-21

<150> JP 1998-300178

<151> 1998-10-21

<160> 18

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 244

<212> PRT

<213> Escherichia coli

<400> 1

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Ile	Gly	Arg	Ala	Ile	Ala	Glu	Thr	Leu	Ala	Ala	Arg	Gly	Ala	Lys	Val	20	25	30	
Ile	Gly	Thr	Ala	Thr	Ser	Glu	Asn	Gly	Ala	Gln	Ala	Ile	Ser	Asp	Tyr	35	40	45	
Leu	Gly	Ala	Asn	Gly	Lys	Gly	Leu	Met	Leu	Asn	Val	Thr	Asp	Pro	Ala	50	55	60	
Ser	Ile	Glu	Ser	Val	Leu	Glu	Lys	Ile	Arg	Ala	Glu	Phe	Gly	Glu	Val	65	70	75	80
Asp	Ile	Leu	Val	Asn	Asn	Ala	Gly	Ile	Thr	Arg	Asp	Asn	Leu	Leu	Met	85	90	95	
Arg	Met	Lys	Asp	Glu	Glu	Trp	Asn	Asp	Ile	Ile	Glu	Thr	Asn	Leu	Ser	100	105	110	
Ser	Val	Phe	Arg	Leu	Ser	Lys	Ala	Val	Met	Arg	Ala	Met	Met	Lys	Lys	115	120	125	
Arg	His	Gly	Arg	Ile	Ile	Thr	Ile	Gly	Ser	Val	Val	Gly	Thr	Met	Gly	130	135	140	
Asn	Gly	Gly	Gln	Ala	Asn	Tyr	Ala	Ala	Ala	Lys	Ala	Gly	Leu	Ile	Gly	145	150	155	160
Phe	Ser	Lys	Ser	Leu	Ala	Arg	Glu	Val	Ala	Ser	Arg	Gly	Ile	Thr	Val	165	170	175	
Asn	Val	Val	Ala	Pro	Gly	Phe	Ile	Glu	Thr	Asp	Met	Thr	Arg	Ala	Leu	180	185	190	
Ser	Asp	Asp	Gln	Arg	Ala	Gly	Ile	Leu	Ala	Gln	Val	Pro	Ala	Gly	Arg	195	200	205	
Leu	Gly	Gly	Ala	Gln	Glu	Ile	Ala	Asn	Ala	Val	Ala	Phe	Leu	Ala	Ser	210	215	220	
Asp	Glu	Ala	Ala	Tyr	Ile	Thr	Gly	Glu	Thr	Leu	His	Val	Asn	Gly	Gly	225	230	235	240
Met	Tyr	Met	Val																

<210> 2

<211> 735

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)...(732)

<400> 2

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Met Asn Phe Glu Gly Lys Ile Ala Leu Val Thr Gly Ala Ser Arg Gly	
1 5 10 15	
att ggc cgc gca att gct gaa acg ctc gca gcc cgt ggc gcg aaa gtt	96
Ile Gly Arg Ala Ile Ala Glu Thr Leu Ala Ala Arg Gly Ala Lys Val	
20 25 30	
att ggc act gcg acc agt gaa aat ggc gct cag gcg atc agt gat tat	144
Ile Gly Thr Ala Thr Ser Glu Asn Gly Ala Gln Ala Ile Ser Asp Tyr	
35 40 45	
tta ggt gcc aac ggc aaa ggt ctg atg ttg aat gtg acc gac ccg gca	192
Leu Gly Ala Asn Gly Lys Gly Leu Met Leu Asn Val Thr Asp Pro Ala	
50 55 60	
tct atc gaa tct gtt ctg gaa aaa att cgc gca gaa ttt ggt gaa gtg	240
Ser Ile Glu Ser Val Leu Glu Lys Ile Arg Ala Glu Phe Gly Glu Val	
65 70 75 80	
gat atc ctg gtc aat aat gcc ggt atc act cgt gat aac ctg tta atg	288
Asp Ile Leu Val Asn Asn Ala Gly Ile Thr Arg Asp Asn Leu Leu Met	
85 90 95	
cga atg aaa gat gaa gag tgg aac gat att atc gaa acc aac ctt tca	336
Arg Met Lys Asp Glu Glu Trp Asn Asp Ile Ile Glu Thr Asn Leu Ser	
100 105 110	
tct gtt ttc cgt ctg tca aaa gcg gta atg cgc gct atg atg aaa aag	384
Ser Val Phe Arg Leu Ser Lys Ala Val Met Arg Ala Met Met Lys Lys	
115 120 125	
cgt cat ggt cgt att atc act atc ggt tct gtg gtt ggt acc atg gga	432
Arg His Gly Arg Ile Ile Thr Ile Gly Ser Val Val Gly Thr Met Gly	
130 135 140	
aat ggc ggt cag gcc aac tac gct gcg gcg aaa gcg ggc ttg atc ggc	480
Asn Gly Gly Gln Ala Asn Tyr Ala Ala Lys Ala Gly Leu Ile Gly	
145 150 155 160	
ttc agt aaa tca ctg gcg cgc gaa gtt gcg tca cgc ggt att act gta	528
Phe Ser Lys Ser Leu Ala Arg Glu Val Ala Ser Arg Gly Ile Thr Val	
165 170 175	
aac gtt gtt gct ccg ggc ttt att gaa acg gac atg aca cgt gcg ctg	576
Asn Val Val Ala Pro Gly Phe Ile Glu Thr Asp Met Thr Arg Ala Leu	
180 185 190	
agc gat gac cag cgt gcg ggt atc ctg gcg cag gtt cct gcg ggt cgc	624
Ser Asp Asp Gln Arg Ala Gly Ile Leu Ala Gln Val Pro Ala Gly Arg	
195 200 205	
ctc ggc ggc gca cag gaa atc gcc aac gcg gtt gca ttc ctg gca tcc	672
Leu Gly Gly Ala Gln Glu Ile Ala Asn Ala Val Ala Phe Leu Ala Ser	
210 215 220	

gac gaa gca gct tac atc acg ggt gaa act ttg cat gtg aac ggc ggg 720
 Asp Glu Ala Ala Tyr Ile Thr Gly Glu Thr Leu His Val Asn Gly Gly
 225 230 235 240

atg tac atg gtc tga 735
 Met Tyr Met Val

<210> 3
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Artificially synthesized primer sequence

<400> 3 36
 aaaggatcca acaatgaatt ttgaaggaaa aatcgc

<210> 4
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Artificially synthesized primer sequence

<400> 4 32
 tgcctcgagt tatcagacca tgtacatccc gc

<210> 5
 <211> 248
 <212> PRT
 <213> Bacillus subtilis

<400> 5
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 1 5 10 15
 Gly Ile Gly Arg Ser Ile Ala Leu Ala Lys Ser Gly Ala Asn
 20 25 30
 Val Val Val Asn Tyr Ser Gly Asn Glu Ala Lys Ala Asn Glu Val Val
 35 40 45
 Asp Glu Ile Lys Ser Met Gly Arg Lys Ala Ile Ala Val Lys Ala Asp
 50 55 60
 Val Ser Asn Pro Glu Asp Val Gln Asn Met Ile Lys Glu Thr Leu Ser
 65 70 75 80
 Val Phe Ser Thr Ile Asp Ile Leu Val Asn Asn Ala Gly Ile Thr Arg
 85 90 95
 Asp Asn Leu Ile Met Arg Met Lys Glu Asp Glu Trp Asp Asp Val Ile
 100 105 110
 Asn Ile Asn Leu Lys Gly Val Phe Asn Cys Thr Lys Ala Val Thr Arg
 115 120 125
 Gln Met Met Lys Gln Arg Ser Gly Arg Ile Ile Asn Val Ser Ser Ile
 130 135 140
 Val Gly Val Ser Gly Asn Pro Gly Gln Ala Asn Tyr Val Ala Ala Lys
 145 150 155 160
 Ala Gly Val Ile Gly Leu Thr Lys Ser Ser Ala Lys Glu Leu Ala Ser
 165 170 175
 Arg Asn Ile Thr Val Asn Ala Ile Ala Pro Gly Phe Ile Ser Thr Asp
 180 185 190

Met Thr Asp Lys Leu Ala Lys Asp Val Gln Asp Glu Met Leu Lys Gln
 195 200 205
 Ile Pro Leu Ala Arg Phe Gly Glu Pro Ser Asp Val Ser Ser Val Val
 210 215 220
 Thr Phe Leu Ala Ser Glu Gly Ala Arg Tyr Met Thr Gly Gln Thr Leu
 225 230 235 240
 His Ile Asp Gly Gly Met Val Met
 245

<210> 6
 <211> 747
 <212> DNA
 <213> Bacillus subtilis

<220>
 <221> CDS
 <222> (1)...(744)

<400> 6
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 Met Asp Met Leu Asn Asp Lys Thr Ala Ile Val Thr Gly Ala Ser Arg
 1 5 10 15
 gga atc ggc cgc tca atc gcc ctt gct ctg gca aaa agc gga gca aat 96
 Gly Ile Gly Arg Ser Ile Ala Leu Ala Lys Ser Gly Ala Asn
 20 25 30
 gtt gtc gtg aac tac tcc ggc aat gaa gcg aaa gca aat gaa gtg gta 144
 Val Val Val Asn Tyr Ser Gly Asn Glu Ala Lys Ala Asn Glu Val Val
 35 40 45
 gat gaa atc aaa tca atg ggc aga aaa gca att gct gta aaa gcg gat 192
 Asp Glu Ile Lys Ser Met Gly Arg Lys Ala Ile Val Lys Ala Asp
 50 55 60
 gta tca aat ccc gaa gat gta caa aac atg ata aaa gaa aca ttg tct 240
 Val Ser Asn Pro Glu Asp Val Gln Asn Met Ile Lys Glu Thr Leu Ser
 65 70 75 80
 gtt ttt tct acg att gac att ctg gtt aat aat gcg gga att aca aga 288
 Val Phe Ser Thr Ile Asp Ile Leu Val Asn Asn Ala Gly Ile Thr Arg
 85 90 95
 gac aat ctc atc atg aga atg aaa gaa gac gaa tgg gat gac gtc att 336
 Asp Asn Leu Ile Met Arg Met Lys Glu Asp Glu Trp Asp Asp Val Ile
 100 105 110
 aac att aac ctg aag ggt gtt ttc aac tgc aca aaa gct gtt aca aga 384
 Asn Ile Asn Leu Lys Gly Val Phe Asn Cys Thr Lys Ala Val Thr Arg
 115 120 125
 caa atg atg aaa cag cgt tca ggc cgc att att aac gta tcg tct atc 432
 Gln Met Met Lys Gln Arg Ser Gly Arg Ile Ile Asn Val Ser Ser Ile
 130 135 140
 gtc ggc gtc agc gga aac cct gga caa gcc aac tac gtg gct gca aaa 480
 Val Gly Val Ser Gly Asn Pro Gly Gln Ala Asn Tyr Val Ala Ala Lys
 145 150 155 160
 gcc ggc gtc atc ggt tta acc aaa tct tct gct aaa gag ctc gcc agc 528
 Ala Gly Val Ile Gly Leu Thr Lys Ser Ser Ala Lys Glu Leu Ala Ser
 165 170 175

cga aat att acg gta aac gca ata gcg cca gga ttt atc tca act gat	576
Arg Asn Ile Thr Val Asn Ala Ile Ala Pro Gly Phe Ile Ser Thr Asp	
180 185 190	
atg aca gat aaa ctt gca aaa gac gtt caa gac gaa atg ctg aaa caa	624
Met Thr Asp Lys Leu Ala Lys Asp Val Gln Asp Glu Met Leu Lys Gln	
195 200 205	
att ccg ctc gcg cgc ttt ggt gaa cct agc gat gtc agc agt gtt gtc	672
Ile Pro Leu Ala Arg Phe Gly Glu Pro Ser Asp Val Ser Ser Val Val	
210 215 220	
acg ttc cta gct tca gag gga gct cgt tat atg aca ggc caa acg ctt	720
Thr Phe Leu Ala Ser Glu Gly Ala Arg Tyr Met Thr Gly Gln Thr Leu	
225 230 235 240	
cat att gac ggc gga atg gtg atg taa	747
His Ile Asp Gly Gly Met Val Met	
245	

<210> 7
 <211> 33
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Artificially synthesized primer sequence

<400> 7
 ggaccatgga tatgcttaat gataaaaacgg cta 33

<210> 8
 <211> 34
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Artificially synthesized primer sequence

<400> 8
 gagaagcttc tcgagttaca tcaccattcc gccg 34

<210> 9
 <211> 246
 <212> PRT
 <213> Ralstonia eutropha

<400> 9
 Met Thr Gln Arg Ile Ala Tyr Val Thr Gly Gly Met Gly Gly Ile Gly
 1 5 10 15
 Thr Ala Ile Cys Gln Arg Leu Ala Lys Asp Gly Phe Arg Val Val Ala
 20 25 30
 Gly Cys Gly Pro Asn Ser Pro Arg Arg Glu Lys Trp Leu Glu Gln Gln
 35 40 45
 Lys Ala Leu Gly Phe Asp Phe Ile Ala Ser Glu Gly Asn Val Ala Asp
 50 55 60
 Trp Asp Ser Thr Lys Thr Ala Phe Asp Lys Val Lys Ser Glu Val Gly
 65 70 75 80

Glu	Val	Asp	Val	Leu	Ile	Asn	Asn	Ala	Gly	Ile	Thr	Arg	Asp	Val	Val
				85					90					95	
Phe	Arg	Lys	Met	Thr	Arg	Ala	Asp	Trp	Asp	Ala	Val	Ile	Asp	Thr	Asn
			100					105					110		
Leu	Thr	Ser	Leu	Phe	Asn	Val	Thr	Lys	Gln	Val	Ile	Asp	Gly	Met	Ala
		115					120					125			
Asp	Arg	Gly	Trp	Gly	Arg	Ile	Val	Asn	Ile	Ser	Ser	Val	Asn	Gly	Gln
		130				135					140				
Lys	Gly	Gln	Phe	Gly	Gln	Thr	Asn	Tyr	Ser	Thr	Ala	Lys	Ala	Gly	Leu
		145			150					155					160
His	Gly	Phe	Thr	Met	Ala	Leu	Ala	Gln	Glu	Val	Ala	Thr	Lys	Gly	Val
				165					170					175	
Thr	Val	Asn	Thr	Val	Ser	Pro	Gly	Tyr	Ile	Ala	Thr	Asp	Met	Val	Lys
			180					185					190		
Ala	Ile	Arg	Gln	Asp	Val	Leu	Asp	Lys	Ile	Val	Ala	Thr	Ile	Pro	Val
		195					200					205			
Lys	Arg	Leu	Gly	Leu	Pro	Glu	Glu	Ile	Ala	Ser	Ile	Cys	Ala	Trp	Leu
		210				215					220				
Ser	Ser	Glu	Glu	Ser	Gly	Phe	Ser	Thr	Gly	Ala	Asp	Phe	Ser	Leu	Asn
		225			230					235					240
Gly	Gly	Leu	His	Met	Gly										
				245											

<210> 10
 <211> 741
 <212> DNA
 <213> *Ralstonia eutropha*

<220>
 <221> CDS
 <222> (1)...(738)

<400> 10 atg act cag cgc att gcg tat gtg acc ggc ggc atg ggt ggt atc gga Met Thr Gln Arg Ile Ala Tyr Val Thr Gly Gly Met Gly Gly Ile Gly 1 5 10 15															48
acc gcc att tgc cag cgg ctg gcc aag gat ggc ttt cgt gtg gtg gcc Thr Ala Ile Cys Gln Arg Leu Ala Lys Asp Gly Phe Arg Val Val Ala 20 25 30															96
ggt tgc ggc ccc aac tcg ccg cgc cgc gaa aag tgg ctg gag cag cag Gly Cys Gly Pro Asn Ser Pro Arg Arg Glu Lys Trp Leu Glu Gln Gln 35 40 45															144
aag gcc ctg ggc ttc gat ttc att gcc tcg gaa ggc aat gtg gct gac Lys Ala Leu Gly Phe Asp Phe Ile Ala Ser Glu Gly Asn Val Ala Asp 50 55 60															192
tgg gac tcg acc aag acc gca ttc gac aag gtc aag tcc gag gtc ggc Trp Asp Ser Thr Lys Thr Ala Phe Asp Lys Val Lys Ser Glu Val Gly 65 70 75 80															240
gag gtt gat gtg ctg atc aac aac gcc ggt atc acc cgc gac gtg gtg Glu Val Asp Val Leu Ile Asn Asn Ala Gly Ile Thr Arg Asp Val Val 85 90 95															288
ttc cgc aag atg acc cgc gcc gac tgg gat gcg gtg atc gac acc aac Phe Arg Lys Met Thr Arg Ala Asp Trp Asp Ala Val Ile Asp Thr Asn 100 105 110															336

ctg acc tcg ctg ttc aac gtc acc aag cag gtg atc gac ggc atg gcc Leu Thr Ser Leu Phe Asn Val Thr Lys Gln Val Ile Asp Gly Met Ala 115 120 125	384
gac cgt ggc tgg ggc cgc atc gtc aac atc tcg tcg gtg aac ggg cag Asp Arg Gly Trp Gly Arg Ile Val Asn Ile Ser Ser Val Asn Gly Gln 130 135 140	432
aag ggc cag ttc ggc cag acc aac tac tcc acc gcc aag gcc ggc ctg Lys Gly Gln Phe Gly Gln Thr Asn Tyr Ser Thr Ala Lys Ala Gly Leu 145 150 155 160	480
cat ggc ttc acc atg gca ctg gcg cag gaa gtg gcg acc aag ggc gtg His Gly Phe Thr Met Ala Leu Ala Gln Glu Val Ala Thr Lys Gly Val 165 170 175	528
acc gtc aac acg gtc tct ccg ggc tat atc gcc acc gac atg gtc aag Thr Val Asn Thr Val Ser Pro Gly Tyr Ile Ala Thr Asp Met Val Lys 180 185 190	576
gcg atc cgc cag gac gtg ctc gac aag atc gtc gcg acg atc ccg gtc Ala Ile Arg Gln Asp Val Leu Asp Lys Ile Val Ala Thr Ile Pro Val 195 200 205	624
aag cgc ctg ggc ctg ccg gaa gag atc gcc tcg atc tgc gcc tgg ttg Lys Arg Leu Gly Leu Pro Glu Glu Ile Ala Ser Ile Cys Ala Trp Leu 210 215 220	672
tcg tcg gag gag tcc ggt ttc tcg acc ggc gcc gac ttc tcg ctc aac Ser Ser Glu Glu Ser Gly Phe Ser Thr Gly Ala Asp Phe Ser Leu Asn 225 230 235 240	720
ggc ggc ctg cat atg ggc taa Gly Gly Leu His Met Gly 245	741

<210> 11
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Artificially synthesized primer sequence

<400> 11
 agtggatcca atgactcagc gcattgcgta 30

<210> 12
 <211> 35
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Artificially synthesized primer sequence

<400> 12
 aacaagcttc tcgagttagc ccatatgcag gccgc 35

<210> 13
 <211> 31
 <212> DNA

<213> Artificial Sequence

<220>
<223> Artificially synthesized sequence

<400> 13
aattctcgag taatctagag gaattctaaa a 31

<210> 14
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificially synthesized sequence

<400> 14
ctagttttag aattcctcta gattactcga g 31

<210> 15
<211> 35
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificially synthesized primer sequence

<400> 15
gaggaattca tacatgtatc cagatttaaa aggaa 35

<210> 16
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificially synthesized primer sequence

<400> 16
ggtaagcttt cattaaccgc ggcttgctg 30

<210> 17
<211> 806
<212> DNA
<213> Bacillus subtilis

<220>
<221> CDS
<222> (12)...(794)

<400> 17
ggaattcata c atg tat cca gat tta aaa gga aaa gtc gtc gct att aca 50
Met Tyr Pro Asp Leu Lys Gly Lys Val Val Ala Ile Thr
1 5 10

gga gct gct tca ggg ctc gga aag gcg atg gcc att cgc ttc ggc aag 98
Gly Ala Ala Ser Gly Leu Gly Lys Ala Met Ala Ile Arg Phe Gly Lys
15 20 25

gag cag gca aaa gtg gtt atc aac tat tat agt aat aaa caa gat ccg 146
Glu Gln Ala Lys Val Val Ile Asn Tyr Tyr Ser Asn Lys Gln Asp Pro
30 35 40 45

aac gag gta aaa gaa gag gtc atc aag gcg ggc ggt gaa gct gtt gtc Asn Glu Val Lys Glu Glu Val Ile Lys Ala Gly Gly Glu Ala Val Val 50 55 60	194
gtc caa gga gat gtc acg aaa gag gaa gat gta aaa aat atc gtg caa Val Gln Gly Asp Val Thr Lys Glu Glu Asp Val Lys Asn Ile Val Gln 65 70 75	242
acg gca att aag gag ttc ggc aca ctc gat att atg att aat aat gcc Thr Ala Ile Lys Glu Phe Gly Thr Leu Asp Ile Met Ile Asn Asn Ala 80 85 90	290
ggt ctt gaa aat cct gtg cca tct cac gaa atg ccg ctc aag gat tgg Gly Leu Glu Asn Pro Val Pro Ser His Glu Met Pro Leu Lys Asp Trp 95 100 105	338
gat aaa gtc atc ggc acg aac tta acg ggt gcc ttt tta gga agc cgt Asp Lys Val Ile Gly Thr Asn Leu Thr Gly Ala Phe Leu Gly Ser Arg 110 115 120 125	386
gaa gcg att aaa tat ttc gta gaa aac gat atc aag gga aat gtc att Glu Ala Ile Lys Tyr Phe Val Glu Asn Asp Ile Lys Gly Asn Val Ile 130 135 140	434
aac atg tcc agt gtg cac gaa gtg att cct tgg ccg tta ttt gtc cac Asn Met Ser Ser Val His Glu Val Ile Pro Trp Pro Leu Phe Val His 145 150 155	482
tat gcg gca agt aaa ggc ggg ata aag ctg atg aca gaa aca tta gcg Tyr Ala Ala Ser Lys Gly Gly Ile Lys Leu Met Thr Glu Thr Leu Ala 160 165 170	530
ttg gaa tac gcg ccg aag ggc att cgc gtc aat aat att ggg cca ggt Leu Glu Tyr Ala Pro Lys Gly Ile Arg Val Asn Asn Ile Gly Pro Gly 175 180 185	578
gcg atc aac acg cca atc aat gct gaa aaa ttc gct gac cct aaa cag Ala Ile Asn Thr Pro Ile Asn Ala Glu Lys Phe Ala Asp Pro Lys Gln 190 195 200 205	626
aaa gct gat gta gaa agc atg att cca atg gga tat atc ggc gaa ccg Lys Ala Asp Val Glu Ser Met Ile Pro Met Gly Tyr Ile Gly Glu Pro 210 215 220	674
gag gag atc gcc gca gta gca gcc tgg ctt gct tcg aag gaa gcc agc Glu Glu Ile Ala Ala Val Ala Ala Trp Leu Ala Ser Lys Glu Ala Ser 225 230 235	722
tac gtc aca ggc atc acg tta ttc gcg gac ggc ggt atg aca caa tat Tyr Val Thr Gly Ile Thr Leu Phe Ala Asp Gly Gly Met Thr Gln Tyr 240 245 250	770
cct tca ttc cag gca ggc cgc ggt taatgaaagc tt Pro Ser Phe Gln Ala Gly Arg Gly 255 260	806

<210> 18
 <211> 261
 <212> PRT
 <213> Bacillus subtilis

<400> 18
 Met Tyr Pro Asp Leu Lys Gly Lys Val Val Ala Ile Thr Gly Ala Ala
 1 5 10 15
 Ser Gly Leu Gly Lys Ala Met Ala Ile Arg Phe Gly Lys Glu Gln Ala
 20 25 30
 Lys Val Val Ile Asn Tyr Tyr Ser Asn Lys Gln Asp Pro Asn Glu Val
 35 40 45
 Lys Glu Glu Val Ile Lys Ala Gly Gly Glu Ala Val Val Val Gln Gly
 50 55 60
 Asp Val Thr Lys Glu Glu Asp Val Lys Asn Ile Val Gln Thr Ala Ile
 65 70 75 80
 Lys Glu Phe Gly Thr Leu Asp Ile Met Ile Asn Asn Ala Gly Leu Glu
 85 90 95
 Asn Pro Val Pro Ser His Glu Met Pro Leu Lys Asp Trp Asp Lys Val
 100 105 110
 Ile Gly Thr Asn Leu Thr Gly Ala Phe Leu Gly Ser Arg Glu Ala Ile
 115 120 125
 Lys Tyr Phe Val Glu Asn Asp Ile Lys Gly Asn Val Ile Asn Met Ser
 130 135 140
 Ser Val His Glu Val Ile Pro Trp Pro Leu Phe Val His Tyr Ala Ala
 145 150 155 160
 Ser Lys Gly Gly Ile Lys Leu Met Thr Glu Thr Leu Ala Leu Glu Tyr
 165 170 175
 Ala Pro Lys Gly Ile Arg Val Asn Asn Ile Gly Pro Gly Ala Ile Asn
 180 185 190
 Thr Pro Ile Asn Ala Glu Lys Phe Ala Asp Pro Lys Gln Lys Ala Asp
 195 200 205
 Val Glu Ser Met Ile Pro Met Gly Tyr Ile Gly Glu Pro Glu Glu Ile
 210 215 220
 Ala Ala Val Ala Ala Trp Leu Ala Ser Lys Glu Ala Ser Tyr Val Thr
 225 230 235 240
 Gly Ile Thr Leu Phe Ala Asp Gly Gly Met Thr Gln Tyr Pro Ser Phe
 245 250 255
 Gln Ala Gly Arg Gly
 260